Appli Appli Appli Appli Appli Appli Appli Appli Appli

18, Appl 6, Appli 1, Appli 30, Appl

Perfect score:

Sequence:

OM protein

е Б

Run

Scoring table:

Minimum DB Maximum DB

Database

```
398 PRIGEIFMIKRCGNGVVEREEQCDCGSVQQCEQDACCLINCTLRPGAACAFGLCCKDCKF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIEH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 FGKDAKSASQNCYKEINSQGNRFGHCGINGTTYLKCHISDVFCGRVQCENVRDIPLLQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08836443
Patent No. 5883241
GENERAL INFORMATION:
APPLICANT: DOCHERTY, Andrew, J.P
APPLICANT: SLOCOMBE, Patrick, M.
APPLICANT: SLOCOMBE, Patrick, M.
APPLICANT: SLOCOMBE, PATRICE, M.
APPLICANT: SLOVENTION: HUMAN METALLOPROTEINASE AND VARIANTS THEREOF
                 sednence
                                                                                                                                                                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%; Score 864; DB 4; Length 72 70.6%; Pred. No. 1.2e-63; ive 24; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2. Application US/09617145
Fatent No. 6485956
GENERAL INFORMATION:
TITLE OF INVENTION: SVPH1-8 DNA and Polypeptides
FILE REFERENCE: 03260.0050-00304
CURRENT FILING DATE: 2000-07-14
FRIOR APPLICATION NUMBER: 60/071,505
FRIOR APPLICATION NUMBER: 61/071,505
FRIOR PILING DATE: 1998-01-14
FRIOR FILING DATE: 1998-01-14
FRIOR FILING PATE: 1998-01-14
FRIOR FILING NOS: 2
SOFTWARE: Patentin Ver. 2.0
US-08-765-243-6
PCT-US95-07295-6
US-08-473-542-2
US-08-477-407-2
US-08-484-355-2
US-08-484-355-1
US-08-447-407-1
US-08-448-355-1
US-09-608-790-1
US-09-026-001A-10
US-09-026-001A-18
                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578 FTLQHTHINGVTCWGIDYHLRMNI 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STVQQFHLNDTTCWGTDYHLGMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.6%
Matches 144; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
                         722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-836-443-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-617-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-617-145-2
                                                                                                                                                    342.5
332.5
312.5
312
312
306.5
283.5
272
272
270.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH:
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
                                                                                                                              August 27, 2004, 21:39:31 ; Search time 21 Seconds (without alignments) 501.509 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15,
Sequence 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                      US-10-633-202-2_COPY_399_602
1192
1 PYPGNI FRLKYCGNLVVEEG......QFHLNDTTCWGTDYHLGMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-351-414-2
US-08-43-542-3
US-08-447-407-3
US-08-447-407-3
US-08-447-407-4
US-08-447-407-4
US-09-48-255-4
US-09-786-256C-32
US-08-26-111-4
US-08-26-111-4
US-08-26-111-4
US-08-26-111-4
US-08-26-111-4
US-08-26-111-4
US-08-26-111-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-836-443-3
US-09-548-797B-5
US-09-632-098-2
US-09-632-098-2
US-09-913-819-4
US-09-920-048-2
US-09-920-048-2
US-09-920-048-2
US-09-26-048-2
US-08-264-101-2
US-08-26-101-2
US-08-765-243-2
US-08-765-243-8
US-08-765-243-8
US-08-765-243-8
US-08-765-243-8
US-08-765-243-8
US-08-765-243-8
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-617-145-2
US-08-836-443-3
US-09-548-797B-5
                                                                                                                                                                                                                                                                                                                                         389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
```

577

Score

Result

Gape

ö

```
Query Match
Best Local Similarity 41.3*
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Conservative
                                                                                                               ; ORGANISM: Homo sapiens
US-09-548-7978-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-632-098-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-632-098-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586
                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 CGNGYLEDGEECDCGEEEEC-NNPCCNASNCTIRPGAECAHGSCCHQCKILAPGTICREQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 VGECDL/PEWCNGTSHQCPDDVYVQDGISC-NVNAFCYEKTCNNHDIQCKEIFGQDARSAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 ARQCDLPEFCTGKSPHCPTNFYQMDGTPCEGGQAYCYNGMCLTYQEQCQQLWGPGARPAP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 QSCYQEINTQGNRFGHCG-IVGTTYVKCWTPDIMCGRVQCENVGVIP---NLIEHSTVQQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09548797B
Patent No. 6683165
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: OBESITY
FILE REFERENCE: 2976-4039
CURRENT APPLICATION NUMBER: US/09/548,797B
CURRENT APPLICATION NUMBER: US/09/548,797B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 CGNLVVEEGEECDCGTIRQCAKDPCC-LLNCTLHPGAACAFGICCKDCKFLPSGTLCRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.2%; Score 431.5; DB 2; Length Best Local Similarity 41.3%; Pred. No. 6e-28; Matches 81; Conservative 29; Mismatches 79; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP STREET: 130 Water Street
                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Disketre
COMPUTER: Disketre
COMPUTER: Disketre
COMPUTER: IBM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/836,443
FILING DATE: 01-MAY-1997
CLASSIFICATION NUMBER: 9709420
FILING DATE: 05-SEP-1997
APPLICATION NUMBER: 9612145.4
FILING DATE: 11-JUN-1996
APPLICATION NUMBER: 9526230.9
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Resmick, David S.
DECT: COMPATION NUMBER: 30.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 47424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 FHLNDTTCWGTDYHLG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNGRQIQCRGTHVYRG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: No. 5883241e
                                                     CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-548-797B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-836-443-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
```

```
409 PDPGLPVPPALCGNGFVBAGEBCDCGPGQBC-RDLCCFAHNCSLRPGAQCAHGDCCVRCL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                    60 FLPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISC-NVNAFCYEKTCNNHDIQCK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 FLPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISC-NVNAFCYEKTCNNHDIQCK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIFGODARSASOSCYQEINTQGNRFGHCGIVGT-TYVKCWTPDIMCGRVQCENVGVIPNL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::| : |::|: |:||: |:||: |::|
528 QLWGPGSHPAPEACFQVVNSAGDAHGNCGQDSEGHFLPCAGRDALCGKLQCQ--GGKPSL 585
                                                                                                                                                                                                                                                                                                                                       1 PYPGNIFRLKYCGNLVVEBGEBCDCGTIRQCAKDPCCLL-NCTLHPGAACAFGICCKDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLL-NCTLHPGAACAFGICCKDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.4%; Score 422.5; DB 4; Length 802; 41.3%; Pred. No. 3.6e-27; tive 36; Mismatches 68; Indels 17
                                                                                                                                                                                                                                            DB 4; Length 787;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
                                                                                                                                                                                                                                         35.4%; Score 422.5; DB 4
41.3%; Pred. No. 3.5e-27;
tive 36; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IE-----HSTVOOFHIN--DITCWG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 IE-----HSTVQOFHLN--DTTCWG 195
PRIOR APPLICATION NUMBER: 60/129,391
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09632098; Patent No. 6420154; GENERAL INFORMATION:
```

```
August 27, 2004, 21:28:15; Search time 128 Seconds (without alignments) 450.310 Million cell updates/sec
                                                                                                                                                                                                                            1 PYPGNIFRLKYCGNLVVEEG......QFHLNDTTCWGTDYHLGMAI 204
                                                                                                                                                                                                                                                                                                                                                             1586107
 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        1586107 segs, 282547505 residues
Copyright (c) 1993 - 2004
                                                                                                                                                                                    US-10-633-202-2_COPY_399_602
1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geneseqp20028; *
geneseqp2003as; *
geneseqp2003bs; *
geneseqp20048; *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_29Jan04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                   | Aay17413 Human SVP | Aay03223 Amino aci | Adc78877 Human PRO | Abr39425 Human GEN | Aay17414 SVPH1-26 | Aae13056 ADAM-20di | Aay03224 Amino aci | Aay28655 Human SVP | Abg76200 Human sna | Aae13057 ADAM-21di | Aab07739 A snake v | Aab07740 A snake v | Aab07741 A snake v | Aae13061 ADAM-29di | Aab07738 A snake v | Aab07743 A snake v | Aab07742 A snake v | Aab07705 Amino aci | Aau12273 Human PRO | Abol7717 Novel hum | Abu80971 Human PRO | Abu66671 Human PRO | Abu59752 Novel sec | Abo24942 Human sec | Abu66947 Human sec |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ΩΙ                            | AAY17413           | AAY03223           | ADC78877           | ABR39425           | AAY17414          | AAE13056           | AAY03224           | AAY28655           | ABG76200           | AAE13057           | AAB07739           | AAB07740           | AAB07741           | AAE13061           | AAB07738           | AAB07743           | AAB07742           | AAB07705           | AAU12273           | AB017717           | ABU80971           | ABU66671           | ABU59752           | ABO24942           | ABU66947           |
| 80                            | 8                  | ~                  | ^                  | ø                  | 7                 | 4                  | ~                  | ~                  | 9                  | 4                  | ო                  | m                  | m                  | 4                  | m                  | ო                  | m                  | m                  | 4                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  |
| %<br>Query<br>Match Length DB | 726                | 726                | 726                | 176                | 535               | 535                | 542                | 722                | 722                | 523                | 166                | 787                | 820                | 528                | 499                | 781                | 790                | 790                | 790                | 790                | 790                | 790                | 790                | . 790              | 790                |
| &<br>Query<br>Match           | 100.0              | 100.0              | 100.0              | 100.0              | 94.6              | 94.6               | 72.5               | 72.5               | 72.5               | 70.5               | 66.1               | 66.1               | 66.1               | 64.8               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               | 49.5               |
| Score                         | 1192               | 1192               | 1192               | 1192               | 1128              | 1128               | 864                | 864                | 864                | 840                | 788                | 788                | 788                | 773                | 590.5              | 590.5              | 590.5              | 90.                | 590.5              | 590.5              | 90.                | 590.5              | 90.                | 590.5              | 590.5              |
| Regult<br>No.                 | -                  | 7                  | m                  | 4                  | ß                 | 9                  | 7                  | 80                 | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 |

| Ada45723 Novel hum Ada76154 Human PRO Ada18804 Human PRO Ada61427 Homo sapi Adb19212 Novel hum Adb19212 Novel hum Adb15795 Human PRO Ada86232 Novel hum Ada6732 Human PRO Ada67377 Human PRO Ada67377 Human PRO Ada67377 Human PRO Ada67377 Human PRO Ada69682 Human PRO Ada68682 Human PRO Ada96892 Human PRO Ada96892 Human PRO Ada96892 Human PRO Ada679195 Human PRO Ada679195 Human PRO Ada96892 Human PRO Ada679195 Human PRO Ada679195 Human PRO | Human<br>Novel<br>Human<br>Novel                        |
|---|---|
| ADA45723<br>ADA76154<br>ADA6154<br>ADB418004<br>ADB41212<br>ADB37753<br>ADB467377<br>ADB47582<br>ADB47582<br>ADB47582<br>ADB47582<br>ADB47582<br>ADB47599   | ADB16537<br>ADB1629<br>ADB14692<br>ADB18653<br>ADB18668 |
|   | ουουο   |
| 7   | 790 790 790 790 790 790 790 790 790 790                 |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4   | . 4 4 4 4 4<br>0 0 0 0 0<br>1 0 0 0 0                   |
|   |   |
|   | , N N N N N N   |
| 00000000000000000000000000000000000000  | . 4 4 4 4 4<br>5 4 5 6 6 7                              |

# ALIGNMENTS

RESULT 1

Human; SVPH1-26; proteinase; testis; fertilisation; spermatogenesis; birth control; detergent additive; diagnosis; testicular cancer. AAY17413 standard; protein; 726 AA. (first entry) Human SVPH1-26 protein. 26-JUL-1999 AAY17413; AAY17413 

Homo sapiens. WO9923228-A1. 98WO-US022965. 97US-0063571P. 30-OCT-1998; 30-OCT-1997;

14-MAY-1999.

(IMMV ) IMMUNEX CORP. Cerretti DP;

WPI; 1999-337487/28. N-PSDB; AAX56461 New human SVPH1-26 DNA useful for the diagnosis and prognosis testicular cancers.

ğ

Claim 2; Page 73-83; 96pp; English.

The present sequence is human SVPH1-26. Human SVPH1-26 polypeptides are proteinases implicated in fertilisation and spermatogenesis. They can be used as therapeutic agents. A proteinase inhibitor of the catalytic domain would inhibit SVPH1-26 activity and would be useful as a method for birth control. Also, an inhibitor of the disintegrin domain of SVPH1-26 may affect fertilisation. The proteinase activity of SVPH1-26 can also be used as a detergent additive for the removal of stains having a protein component. The SVPH1-26 polypeptides and fragments can also be used as molecular weight markers, as markers for determination of isoelectric points of sample proteins and as controls for establishing the extent of fragmentation of a protein sample. The products can also be used for identifying, separating or purifying cells that express SVPH1-26 used for identifying, separating or purifying cells that express SVPH1-26 polypeptides such as testis cells. They can be used for the diagnosis and

ö

Gaps

458

578

ប្តង្គន្ល

g ò g 8 셤 à ద

ਨੇ

```
LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEXTCNNHDIQCKEI 120
                                                                                                                                                                                                                                               FGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIEH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of human PRO proteins. The DNA and protein sequences of the invention are useful for the diagnosis and treatment of cancer and inflammatory bowel disease (e.g. ulcerative colitis or Crohn's disease). The present amino acid sequence represents a human PRO protein of the invention.
                                                                                                                                                                                                                                                                      PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAXDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PYPGNIFRLKYCGNLVVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                       PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                            LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; inflammatory bowel disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polynucleotide and polypeptide, useful for the manufacture medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.
                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1192; DB 7; Length 726; 100.0%; Pred. No. 8.4e-88; ive 0; Mismatches 0; Indels 0
                                Length 726;
                                                                    Indels
                                100.0%; Score 1192; DB 2;
100.0%; Pred. No. 8.4e-88;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; SEQ ID NO 106; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                    602
                                                                                                                                                                                                                                                                                                                  STVOOFHLNDTTCWGTDYHLGMAI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC78877 standard; protein; 726 AA.
                                                                                                                                                                                                                                                                                                                                    STVQQFHLNDTTCWGTDYHLGMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-2002; 2002WO-US033070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-OCT-2001; 2001US-0340083P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarry
hes 204; Conservative
                                                Best Local Similarity 100.
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO protein #53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-481990/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADC78876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 726 AA;
Sequence 726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003034984-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC78877;
                                                                                                       ч
                                                                                                                                                                          61
                                                                                                                                                                                                            459
                                                                                                                                                                                                                                                                               519
                                                                                                                                       399
                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                    579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       ADC78877
ID ADC
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
 g
                                                                                                         à
                                                                                                                                    g
                                                                                                                                                                          8
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a amino acid sequence of the novel membrane metalloprotease protein designated ADAM 16a, isolated from human testis, and used in the method of the invention. It may be used in contraceptive, vaccines, or in fertility diagnosis and treatment. It may be involved sperm maturation, or fertilisation through mechanisms such as proteolysis, cell adhesion, cell fusion, or intracellular signalling
                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                  578
                                                                                                                                                                          458
                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane metalloprotease protein; human; ADAM 16a; testis; contraceptive; vaccine; fertility diagnosis; fertility treatment.
                                                                                                                                                             399 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKOPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                                                                 FGQDARSASQSCYQE1NTQGNRFGHCG1VGTTYVKCWTPD1MCGRVQCENVGV1PNL1EH
                                                                                                                                                                                                                                                                                                     519 FGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIEH
                                                                                                                                       1 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                               459 LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAPCYEKTCNNHDIQCKEI
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New metalloprotease proteins ADAM16a and ADAM16b - useful in contraception, and in the evaluation and treatment of fertility.
                                                                                                       ;
                                                                      726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the novel metalloprotease ADAM 16a
                                                                      Length
                                                                                                     Indels
                                                                 Score 1192; DB 2;
Pred. No. 8.4e-88;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32. .727
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                    STVOOFHLNDTTCWGTDYHLGMAI 204
                                                                                                                                                                                                                                                                                                                                                                        STVQQFHLNDTTCWGTDYHLGMAI 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY03223 standard; protein; 726
 prognosis of testicular cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 3A; 59pp; English.
                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-EP004859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-00016755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hooft Van Huijsduinen RAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190050/16.
N-PSDB; AAX28636.
                                                                   Query Match
Best Local Similarity
                                  Sequence 726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9907856-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1998;
                                                                                                   204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999.
                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY03223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY03223
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
```

ö

Gaps

ಡ

ŏ

9

P70535 rattus norv

```
Q28484 macaca fasc
Q28485 macaca fasc
Q28485 macaca fasc
Q28659 oryctolagus
Q28477 macaca fasc
Q28477 macaca fasc
Q28476 macaca fasc
Q46652 papio anubi
Q28476 macaca fasc
Q46652 papio anubi
Q19050 oryctolagus
Q19057 pongo pygma
Q60410 cavia porce
P97777 rattus norv
Q80410 cavia porce
P97777 rattus norv
Q80416 cavia porce
Q77634 sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8n0w6 homo sapien
077635 bos taurus
Q967h9 strongyloce
Q8uvf2 coturnix co
Q9ga15 drosophila
Q9vx11 drosophila
                        0951w7 macaca fasc
019051 oryctolagus
042593 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228483 macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q866a8 sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Choi I., Cho C.;

"Choing and characterization of ADAM29.";

"Cloning and characterization of ADAM29.";

"Considering and characterization of ADAM29.";

EMBL, AV190759; AA038663.1; -.

SO, GO:0004222; F:metalloendopeptidase activity; IEA.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

RI THEFPC; IPR00588; ADAM Cysteine.

InterPrc; IPR001563; Deptidase_M12B.

InterPrc; IPR001563; Peptidase_M12B.

IN ETERPC; IPR002870; Peptidase_M12B.N.

Pfam; PF01421; Reprolysis; 1.

R Pfam; PF01421; Reprolysis; 1.

R PFMNTS; PR00289; DISINTEGRIN.

R PRINTS; PR00289; DISINTEGRIN.

R PRINTS; PR00289; DISINTEGRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00608; ACR; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
SEQUENCE 763 AA; 86444 MW; P9EF082C3BFBBAR0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 753; DB 11;
Pred. No. 5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
  P70535
09951W7
019051
042593
0426484
028484
019061
028476
028476
028476
019050
019050
019050
019050
007777
0810777
0017779
0077634
019057
0077634
019057
0077634
019057
0077634
019057
019050
019057
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
019050
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ul-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 25, ADAM29.
                                                                                                                                                                                                                                                                                                                                              1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q811Q4;
Q811Q4;
Q1-JUN-2003
489.5
485.5
476
468.5
466.5
466.5
466.5
                                                                                                                                                                                                              464
463.5
459.5
451.5
450
448
                                                                                                                                                                                                                                                                                                                                                                440
438.5
                                                                                                                                                                                                                                                                                                                                                                                                          428
427
426
422.5
422.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413
407.5
407.5
402.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
Q811Q4
  Q81194 mus musculu QBcdv3 mus musculu QBcdv3 mus musculu QBk4k0 mus musculu QBkbx7 homo sapien Q42595 xenopus lae Q41072 mus musculu QB0094 mus musculu QBcdv3 mus musculu QBcdy1 mus musculu QBcgy1 aus mu
                                                                                                                                       August 27, 2004, 21:35:56; Search time 116 Seconds (without alignments) 554.877 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                             US-10-633-202-2_COPY_399_602
1192
1 PYPGNIFRLKYCGNLVVEEG......QFHLNDTTCWGTDYHLGMAI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                              1017041
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                  1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q811Q4
Q8CDV3
Q8BMR5
Q8K4K0
Q8BMR4
Q8TBZ7
Q42595
Q61072
Q80U94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            081103
08C0V3
08CG01
060815
08CG02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sparches:
sparches:
sparches:
spacetris:
sphuman:
sphuman:
sphuman:
spmc:
sporganelle:
spphage:
spprodent:
spprodent:
sprodent:
spvortebrate:
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11114111111111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763
761
702
702
702
703
873
885
703
703
703
703
703
703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
```

Result No.

Minimum DB seq Maximum DB seq

Database :

Title: Perfect score:

Seguence:

OM protein

Run on:

Scoring table:

Searched:

```
RA The FANTOM Consortium,

RA The FANTOM Consortium,

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of

RT (6,770 full-length CDNAs.";

RY Nature 420:563-573(2002).

REMBL, AKO2599, BAC56524.1; -.

BR MGD; MG1:2181992; Adam34.

RO; GO:00004222; F:metalloendopeptidase activity; IEA.

RO; GO:00004220; F:metalloendopeptidase activity; IEA.

RO; GO:00004220; F:metalloendopeptidase activity; IEA.

RO; GO:0000520; P:metalloendopeptidase activity; IEA.

RO; GO:0000520; P:metalloendopeptidase activity; IEA.

RO; GO:0000520; P:metalloendopeptidase activity; IEA.

BR HOROSOS; P:metalloendopeptidase activity; IEA.

BR ROSOSOS; P:metalloendopeptidase activity; IEA.

BR RINTS; PRO0020; D:miregrin; 1.

BR Pfam; PF01562; Pep_M12B, Propep; 1.

BR Pfam; PF01562; Pep_M12B, Propep; 1.

BR PROSITE; PS00209; DISINTEGRIN; 1.

BR ROSITE; PS00427; DISINTEGRIN; 1.

BR ROSITE; PS00427; DISINTEGRIN; 1.

BR ROSITE; PS00427; DISINTEGRIN; 1.

BR ROSITE; PS00143; ZINC PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 NECDLPEWCNGTSAECPGDVYKADGIPCSGEGYCYKMECHQRDEQCRKIFGNGSRSADEI 517
                   120 IFGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIE 179
                                      CYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIEHSTVQQFHLNDT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GECDLPEWCNGTSHOCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEIFGQDARSASQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                          (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 664; DB 11; 54.4%; Pred. No. 1.6e-62; iive 33; Mismatches 55;
                                                                                                                                                                                                                       702 AA
                                                                                                               | |: | :|| |||||||| | HYTIHWTHFNSVSCWSTDYHLGMKI 602
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
                                                                                            180 HSTVQOFHLNDTTCWGTDYHLGMAI
                                                                                                                                                                                                                                                                                                                     Similar to ADAM 26 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 54.48
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCWGTDYHLGMAI 204
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                           01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                  01-OCT-2003
                                                                                                                              578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                           Q8BMR5
                                                                                                                                                                                      RESULT
Q8BMR5
                   Š
                                                g
                                                                                          ò
                                                                                                                             g
                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC SEQUENCE FROM N.A.

RC STRAIN=CSTBL/6J, TISSUE=Teetis;

RX The FRATYOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

RA The FRATYOM Consortium,

RA The FRATOM Consortium,

RY "Analysis of the mouse transcriptome based on functional amotation of 60,70 full-length CDNAs.";

REMBL; AK029528; BAC26497.1; -.

DR GO; GO:0006229; F:metalloendopeptidase activity; IEA.

BR GO; GO:0006229; F:metalloendopeptidase activity; IEA.

GO; GO:0006209; P:proceolyais and peptidolysis; IEA.

BR GO; GO:0006209; P:proceolyais and peptidolysis; IEA.

BR InterPro; IPR001876; Disintegrin.

BR InterPro; IPR00280; D:peptidase_M12B.

BR InterPro; IPR00280; Peptidase_M12B.

BR InterPro; IPR00280; Peptidase_M12B.

BR InterPro; IPR00280; Peptidase_M12B.

BR InterPro; IPR00280; Peptidase_M12B.

BR InterPro; IPR00280; D:peptimicagrin; 1.

BR Fam; PF00200; disintegrin; 1.

BR FAMAT; SM000664; Disintegrin; 1.

BR PROSITE; PS00142; RADAM MEPRO; 1.

BR PROSITE; PS00142; ZING PROTEASE; 1.
 ö
                                                                                                                                                  515
                                                         62 PSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEIF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 FLPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 IQPSGTLCRARENECDLPEWCNGTSHECPEDLFVQDGTSCPGDGYCYEKRCNSHDVHCQR 517
                                    2 YPGNIFRLKYCGNLVVEBGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKFL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICC-KDCK 59
                                                                                                                                456 PSGTLCRKRDNICDLPEWCNGTSHECPDDAYVEDGIPGGVSAYCYEKQCNDRNEHCRQIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.3%; Score 718.5; DB 11; Length 761; Best Local Similarity 55.6%; Pred. No. 2.5e-68; Matches 114; Conservative 36; Mismatches 54; Indels 1;
43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
A disintegrin and matalloprotease domain 24.
Mus musculus (Mouse).
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          761 AA
                                                                                                                                                                                                                                                           182 TVQQFHLNDTTCWGTDYHLGMAI 204
                                                                                                                                                                                                                                                                                 576 TIHFALVKNVSCWGTDYHTGTSL 598
119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          QBCDV3;
                                                                                                                                                                                                                                                                                                                                                                                          Q8CDV3
Matches
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                      ð
                                                                       g
                                                                                                             ઠે
                                                                                                                                          ď
                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

ö

131

```
5.1.6
Compugen Ltd.
version :
- 2004 (
GenCore (c) 1993
         Copyright
```

| model   |  |
|---------|--|
| 38      |  |
| using   |  |
| search, |  |
| protein |  |
| •       |  |
| otein   |  |
| M pr    |  |
|         |  |

August 27, 2004, 21:38:21; Search time 40 Seconds (without alignments) 490.577 Million cell updates/sec Run on:

US-10-633-202-2\_COPY\_399\_602 1192 Title: Perfect score:

1 PYPGNIFRLKYCGNLVVEEG......QFHLNDTTCWGTDYHLGMAI 204 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* . . . .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | de    |        |    | SUMMARIES |                    |
|---------------|-------|-------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query | Length | DB | ID        | Description        |
| -             | 567   | 47.6  | 655    | 10 | JC7850    | disintegrin and me |
| 8             | 536.5 | 45.0  | 99     | ~  | S71949    | metalloproteinase  |
| ٣             | 502.5 | 42.2  |        | N  | I49283    | ADAM 4 protein pre |
| 4             | 501.5 | ς.    | 735    | ~  | 148101    | ADAM 6 protein pre |
| Z.            | 468.5 | •     | 732    | ~  | u,        | testicular metallo |
| 9             | 467.5 |       | 713    | ~  | I65253    | disintegrin-like t |
| 7             | 464   |       | 825    | N  | G)        | fertilin alpha-II  |
| 80            | 464   | 38.9  | 905    | ~  | S55059    |                    |
| 0             | 442   | 37.1  | 9      | ~  | I49281    |                    |
| 10            | 425.5 | 35.7  | 903    | ~  | S60257    |                    |
|               | 417.5 | 2     | 151    | N  | 860259    | meltrin gamma - mo |
| 12            | 402.5 | 33.8  | 756    | ~  | 847656    | tMDC II protein -  |
| 13            | 401.5 |       | 814    | ~  | G02390    | σ                  |
| 14            | 391.5 | 2     | 777    | 7  | I48100    | ADAM 5 protein pre |
| 15            | 390   | ς.    | 734    | N  | JC4861    | fertillin beta cha |
| 16            | 386.5 | •     | 176    | N  | S28258    | androgen-regulated |
| 17            | 384   | 32.2  | 670    | ~  | 165967    | disintegrin-like m |
| 18            | 375   | ä     | 735    | ~  | G02937    | fertilin beta - cr |
| 19            | 374   | ä     | 789    | N  | S28259    | androgen-regulated |
| 20            | 372   | ä     | 571    | ~  | S24789    | jararhagin C precu |
| 21            | 371   | 31.1  | 609    | ~  | 855270    | catrocollastatin p |
| 22            | 369   | ä     | 419    | ~  | A59414    | metalloproteinase  |
| 23            | 367   | ö     | 150    | N  | \$60258   | meltrin beta - mou |
| 24            | 359   | •     | 429    | ~  | A42972    | coagulation factor |
| 25            | 357.5 | ö     | 357    | ~  | S23403    | sperm surface prot |
| 26            | 26    | 29.9  | 952    | ~  | T18900    | disintegrin and me |
| 27            | 354   | ٩.    | 617    | ~  | S48160    | metalloproteinase  |
| 28            | 353   |       | 610    | ~  | 753       | vascular apoptosis |
| 53            | 347   | 29.1  | 524    | ~  | S38539    | disintegrin-like m |

| hypothetical prote<br>hemorrhagic protei<br>tMDC I protein - c | ecarin precursor -<br>platelet aggregati<br>platelet aggregati | atrolysin A (EC 3.<br>monocyte surface a<br>cyritestin precurs<br>metalloproteinase | probable zinc meta<br>sperm surface prot<br>bitan alpha - puff | trigramin precurso<br>applaggin - easter<br>albolabrin - green |
|--|--|---|--|--|
| 7.7  | 200  | 9887  | 222  | 300<br>1   |
| T26644<br>A37877<br>S47645                                     | AS579<br>JX026<br>JX026  | S41607<br>A60385<br>S18968<br>S48169  | T3781<br>S2340<br>F3598  | A3399<br>A2373   |
| 000  | 0000   | 0000  | 000  | H W W  |
| 1042<br>416<br>736   | 616<br>209<br>216  | 819<br>826<br>549   | 512<br>289<br>83   | 480<br>71<br>73  |
| 28.9<br>28.4<br>3.4  | 27.9   | 27.5<br>26.6<br>25.1  | 22.3<br>20.8<br>16.7   | 16.4<br>16.3<br>15.9   |
| 345<br>338<br>337  | 332.5  | 327.5<br>324<br>317<br>299.5  | 266<br>248<br>198.5  | 196<br>194.5<br>190  |
| 30<br>31   | 6 4 5 6  | 33 3 4 6<br>3 8 8 4 6   | 0 4 4<br>0 1 2   | 4 4 4<br>6 4 7   |

### ALIGNMENTS

| 걾 | 920 |
|---|-----|
| _ |     |
|   |     |
|   |     |
|   |     |
|   |     |
|   |     |

disintegrin and metalloproteinase(ADAM) 9 protein, short form - human N;Alternate names: MDC9 protein; meltrin gamma C;Species: Homo sapiens (man) C;Species: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 31-Mar-2003 C;Accession: JC7850

Finctoda, N.; Koike, H.; Sasagawa, N.; Ishiura, S.
Blochem. Blophys. Res. Commun. 293, 800-805, 2002
A;Title: A secreted form of human ADAM9 has an alpha-secretase activity for APP.
A;Reference number: JC7850; MUID:22050095; PMID:12054541
A;Accession: JC7850
A;Accession: JC7850
A;Residues: 1-655 <HOT>
A;Residues: 1-655 <HOT>
A;Cross-references: GB:AF495383
A;Cross-references: GB:AF495383
C;Comment: This protein, which is a member of the a disintegrin and metalloprotease (AD:C)Gument: This protein; and has an alpha-secretase activity for C;Genetics:

A;Gene: adam9s

Gaps 14; Query Match 47.6%; Score 567; DB 2; Length 655; Best Local Similarity 46.4%; Pred. No. 1.8e-36; Matches 97; Conservative 36; Mismatches 62; Indels

406 PKPDEAYSAPSCGNXLVDAGEECDCGTPKECELDPCCEGSTCXLKSFAECAYGDCCKDCR 465 1 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCL-LNCTLHPGAACAFGICCKDCK ò g

60 FLPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISC-NVNAFCYEKTCNNHDIQCK 118 Š

a

EIFGODARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENV----G 172 119 ઠે g

δ

VIPNLIEHSTVOOFHLNDTTCWGTDYHLG 201 173 셤

metalloproteinase 12 (EC 3.4.24.-) precursor - human NyAlternate names: disintegrin 12; myeloma cell metalloproteinase MCMP (5.5pecies: Homo sapiens (man) (5.5pecies: Homo sapiens (man) (5.5pecies: Homo sapiens (man) (5.5pecies: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 04-Feb-2000 (5.Accession: S71949; PC4264 (Manards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I. Biochem. J. 318, 459-462, 1996 Membrane-linked metalloproteinase from human myeloma cells. A;Reference number: S71949; MUID:96404892; PMID:8809033

~

```
Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I48101
                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                    ò
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-660 «WCX>
A;Ricle: Expression of members of a novel membrane linked metalloproteinase family (ADAM A;Reference number: PC4264; MUD:97168971; PMID:9016778
A;Recession: PC4264
A;Recession: PC4264
A;Recession: PC4264
A;Recence number: PC4263; MUD:97168971; PMID:9016778
A;Residues: 1-337 «MCP>
A;Residues: 1-34 «MCP>
A;Residues: 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 PKPDEAYSAPSCGNKLVDAGEECDCGTPKECELDPCCEGSTCKLKSFAECAYGDCCKDCR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISC-NVNAFCYEKTCNNHDIQCK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 FLPGGTLCRGKTSECDVPEYCNGSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYYDAQCQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIFGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWT-----------158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PDIMCGRVQCENV-----GVIPNLIEHSTVQQFHLN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 VIFGSKAKAAPKDCFIEVNSKGDRFGNCGFSGNEYKKCATGLSLKFHAPFLSTMLQEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTYLGGSVCCMKSDCRIVTLVKNALCGKLQCENVQBIPVFGIVPAIIQTPS-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAXDPCCL-LNCTLHPGAACAFGICCXDCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.5%; Pred. No. 4e-34;
Matches 97; Conservative 36; Mismatches 62; Indels 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || || |: ||
GTKCWGVDFQLG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DITCWGTDYHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ADAM 6 protein precursor - guinea pig
C.Species: Cavia porcellus (guinea pig)
C.Species: Cavia porcellus (guinea pig)
C.Accession: 148101
R.Molfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.
Por. Biol. 169, 378-383, 1995
A.Title: ADAM, a widely distributed and developmentally regulated gene family encoding manager. Description of the procession of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 testicular metalloproteinase-like, disintegrin-like, cysteine-rich protein IVa - crab-ea C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Oz-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 21-Uul-2000
C;Accession: 152361
R;Perry, A.C.F.; Jones, R.; Hall, L.
B;ochem. J. 312, 239-244, 1995
A;Title: Analysis of transcripts encoding novel members of the mammalian metalloproteasc octive monkey tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 VGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEIFGQDARSASQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLCROQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEIFGQD 124
                                                                                                                                                                                                                                                                                                                                                                                                                     125 ARSASQSCYQEINTQGNRFGHCGI----VGTTYVKCWTPDIMCGRVQCENVGVIPNLIEH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 VXDGSPACYNELAVKGDRFGNCGIGIIRGSQPVPCQKEDVFCGMIHCDGVSHIPGGGEH 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCYQEINTQGNRFGHCGIVGT--TYVKCWTPDIMCGRVQCENVGVIPNLIEHSTVQQFHL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 NIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKFLPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: U22061; NID: 9965007; PIDN: AAA74919.1; PID: 9965008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
    Length
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ADAM6
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;404-486/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                                         77;
    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 501.5; DB 2
Pred. No. 2.2e-31;
42.2%; Score 502.5; DB 2
41.2%; Pred. No. 1.3e-31;
ive 36; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
42.1%; Score 501.5; 1
Best Local Similarity 44.5%; Pred. No. 2.2e
Matches 85; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTFYHLKVQDVKEEQCFGYDAHHG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STVQQFHLNDT---TCWGTDYHLG 201
                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDTTCWGTDYH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 GNSWCFGVDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-735 < RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: I48101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

encoding

ADAM 4 protein precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: 149283

R;Wolfeberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, Ibov. Biol. 169, 378-383; 1995

A;Title: ADAM, a widely distributed and developmentally regulated gene family encoding A;Reference number: 148100; MUID:95269891; PMID:7750654

A;Recession: 149283

A;Rectus: prediminary; translated from GB/EMBL/DDBJ

A;Rectus: prediminary;

A;Molecule type: mRNA

A;Rossidues: 1-473 <RES>

A;Cross-references: EMBL:U22058; NID:9965013; PIDN:AAA74922.1; PID:9965014

149283

A;Gene: ADAM4 C;Superfamily: mouse meltrin alpha; disintegrin homology F;129-211/Domain: disintegrin homology <DIS>

```
August 27, 2004, 21:35:21; Search time 24 Seconds (without alignments) 442.596 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                 Run on:
```

US-10-633-202-2\_COPY\_399\_602 1192 1 PYPGNIFRLKYCGNLVVEEG......QFHLNDTTCWGTDYHLGMAI 204 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description | homod | homo | 5 homo | O9r159 mus musculu | Q9ji76 mus musculu | Q9r160 mus musculu | Q9r158 mus musculu | рошо  | homo       | rattı | Q60813 mus musculu | O43184 homo sapien | Q9h013 homo sapien | mus     | O35674 mus musculu | Q9bz11 homo sapien |       | xeno       | mus   | pog    | แนย แ  | homo  | homo  | -     | ~     |            | _     | -     | Q923w9 mus musculu | Q9psz3 xenopus lae | ᄰ    |       | mus muscul |
|-----------|-------------|-------|------|--------|--------------------|--------------------|--------------------|--------------------|-------|------------|-------|--------------------|--------------------|--------------------|---------|--------------------|--------------------|-------|------------|-------|--------|--------|-------|-------|-------|-------|------------|-------|-------|--------------------|--------------------|------|-------|------------|
|           | į           |       |      |        |                    |                    |                    |                    |       |            |       |                    |                    |                    |         |                    |                    |       |            |       |        |        |       |       |       |       |            |       |       |                    |                    |      |       |            |
| **        |             |       |      | •      |                    |                    |                    |                    |       |            |       |                    |                    |                    |         |                    |                    |       |            |       |        |        |       |       |       |       |            |       |       |                    |                    |      |       |            |
| SUMMARIES |             |       |      |        |                    | MOUSE              | MOUSE              | MOUSE              | HUMAN | AD09 HUMAN | RAT   | AD1A MOUSE         | HUMAN              | HUMAN              | 2 MOUSE | AD19 MOUSE         | HUMAN              | HUMAN | AD22_XENLA | MOUSE | BOVIN  | MOUSE  | HUMAN | HUMAN | MOUSE | RABIT | AD02_HUMAN | MOUSE | MACFA | MOUSE              | XENLA              |      | RAT   | _MOUSE     |
|           | ឧ           | AD20  | AD21 | AD29   | AD25               | AD21               | AD24               | AD26               | AD30  | AD09       | AD01  | ADIA               | AD12               | AD19               | AD12    | AD19               | AD33               | AD22  | AD22       | AD1B  | AD02_B | AD22 N | AD15  | AD07  | AD15  | AD02  | AD02       | AD11  | AD07  | AD33               | AD11               | AD11 | AD15  | AD07       |
|           | <b>图</b>    | П     | -    | -      |                    | -                  | ٦                  | -                  | ч     | -          | н     |                    |                    | -                  | ч       | -                  | -                  | ч     | ч          | П     | -      | -      | Н     | -     | -     | -     | н          | ч     | -     | ч                  | -                  | -    | -     | 7          |
|           | Length      | 726   | 722  | 820    | 760                | 729                | 761                | 697                | 790   | 819        | 789   | 791                | 606                | 926                | 903     | 920                | 813                | 906   | 932        | 908   | 745    | 857    | 814   | 754   | 864   | 751   | 735        | 773   | 176   | 797                | 452                | 769  | 816   | 788        |
|           | Match       |       | 72.5 | ٠.     | 4,                 | 62.7               | ٥.                 | 55.7               | 49.5  | 47.6       | æ     | 7.                 | 37.1               | ė.                 | ů.      | 35.7               | 35.4               | Š.    | 35.3       | 5     | ů.     | 5      | 33.7  | ش     | ä     | Э.    | 32.7       | 'n    | ď     | ď                  | ď                  | 32.2 | ij    | 31.6       |
|           | Score       | 1192  | 864  | 788    | 769                | 747                | 716.5              | 664                | 590.5 | 567        | 461.5 | 450                | 442.5              | 437.5              | 425.5   | 425.5              | 422.5              | 422   | 421        | 420   | 418    | 418    | 401.5 | 399.5 | 399.5 | 395   | 390        | 387   | 386.5 | 386.5              | 385                | 384  | 380.5 | 377        |
| Result    | No.         | ч     | 7    | ю      | 4                  | ιΩ                 | 9                  | 7                  | 80    | თ          | 10    | 11                 | 12                 | 13                 | 14      | 15                 | 16                 | 17    | 18         | 19    |        |        | 22    | 23    | 24    | 25    | 26         | 27    | 28    | 29                 | 30                 | 31   | 32    | 33         |

EMBL; AF029899; AAC52041.1; -.

DR

| Q28478 macaca fasc Q9x816 macaca fasc Q63180 rattus norv P30431 bothrops ja Q9ukq2 homo sapien Q60718 mus musculu Q9j1n6 mus musculu Q60411 cavia porce Q63202 rattus norv Q9y37 homo sapien P20164 trimeresuru Q95194 macaca fasc  |
|---|
| AD02 MACFA<br>AD02 MACFA<br>AD07_MAT<br>DISJ BOTJA<br>AD02_WOUSE<br>AD02_CAVPO<br>AD02_CAVPO<br>AD02_CAVPO<br>AD18_HUMAN<br>HR1B_TR1FL  |
| аннаннанна  |
| 735<br>776<br>778<br>775<br>735<br>737<br>739<br>739<br>746   |
| 331.5<br>311.5<br>311.2<br>311.2<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7<br>310.7 |
|   |
|   |

# ALIGNMENTS

```
459 LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEI 518
                                                                                                                                                                                                                                                                                722 AA
                                                                                                                            204
                                                                                                                                                    STVQOFHLNDTTCWGTDYHLGMAI 602
                                                                                                                              STVQQFHLNDTTCWGTDYHLGMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AFISB644; AAD55255.1; -.
EMBL, AF029900; AAC52042.1; -.
HSSP; P18619; IFVL.
MEROPS; M12.234; -.
                                                                                                                                                                                                                                                                                AD21 HUMAN STANDARD;
Q9UKJ8; O43507;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 181-722 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Testis;
                                          121
                                                                                    519
                                                                                                                              181
                                                                                                                                                                      579
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAM21
                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                      RESULT 2
                                       ò
                                                                                 셤
                                                                                                                            Š
                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPSGTLCRQQVGECDLPEWCNGTSHQCPDDVYVQDG1SCNVNAFCYEKTCNNHD1QCKE1 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PYPGNIFRLKYCGNLVVEEGEECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                          M MIM, 600/122; F. metallopeptidase activity; TAS.

R GO; GO: 0007338; P:fertilization (sensu Animalia); TAS.

R GO; GO: 0007338; P:fertilization (sensu Animalia); TAS.

R InterPro; IPR00586; ADAM cysteine.

R InterPro; IPR001589; Pept Miss.

R InterPro; IPR001899; Pept Miss.

R InterPro; IPR001899; Peptidase_Miss.

R Pfam; PF01562; Pep Miss_prope; 1.

R Pfam; PF01562; Pep Miss_prope; 1.

R Pfam; PF01664; Disintegrin; 1.

R PROSTE; PR00068; ACR; 1.

R PROSTE; PS00129; ADAM_MEPRO; 1.

R PROSTE; PS00129; ADAM_MEPRO; 1.

R PROSTE; PS00129; BGF 2; FALSE NEG.

R PROSTE; PS00142; DISINTEGRIN 1; FALSE NEG.

R PROSTE; PS00142; EGF 2; FALSE NEG.

R PROSTE; PS00142; ZINC_POTEASE; AINC; Signal; Glycoprotein; Zymogen;

M Hydrolase; McE-like Adam;

M Hydrolase; Ref-like; Edf-like Adm;

M Hydrolase; McE-like; Edf-like; Edf-like; Edf-like;

M Hydrolase; McE-like; Edf-like;

M Hydrolase; McE-like;

M Hydrolase; McE-like;

M Hydrolase;

M 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYSTEINE SWITCH.
CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF356A6771CD1C12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAM 20.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1192; DB 1;
100.0%; Pred. No. 2.8e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F (IN REF. 2).
C (IN REF. 2).
P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC (CATALYTIC) (ZINC (CATALYTIC) (ZINC (CATALYTIC) (BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISINTEGRIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81710 MW;
  EMBL; AF158643; AAD55254.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
hes 204; Conservative
                                   MEROPS; M12.218; -. Genew; HGNC:199; ADAM20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
637
726 AA;
                                                                                 603712; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
DORRAR OD DRA BARRAR OD DRA BARRAR OD DRA BARRAR OD BARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
FGQDARSASQSCYQEINTQGNRFGHCGIVGTTYVKCWTPDIMCGRVQCENVGVIPNLIEH 180
                                                 -I- DOWAIN: The cysteine-Tich domain encodes putative cell-fusion peptides, which could be involved in sperm-egg fusion.

-I- PTM: Has no obvious cleavage site for furin endopeptidase, suggesting that the proteolytic processing is regulated.

-I- MISCELLANEONS: May be the functional equivalent of ADAM 1/fertilin alpha which is a pseudogene in human.

-I- SIMILARITY: Belongs to peptidase family M12B.

-I- SIMILARITY: Contains 1 EGF-like domain.

-I- SIMILARITY: Contains 1 disintegrin domain.

-I- CAUTION: The sequence of Ref. 2 has a Tyr at position 345, and thus has been thought to be an inactive metalloprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98137801; PubMed=9469942;

Hooft van Huijsduijnen R.;

"ADAM 20 and 21; two novel human testis-specific membrane
metalloproceases with similarity to fertilin-alpha.";

Gene 206:273-282(1998).

-!- FUNCTION: May be involved in sperm maturation and/or
- FUNCTION: May also be involved in epithelia functions
associated with etablishing and maintaining gradients of ions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
ADAM 21 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
domain 21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99453762; PubMed=10524237;
Poindexter K., Nelson N., DuBose R.F., Black R.A., Cerretti D.P.;
"The identification of seven metalloproteinase-disintegrin (ADAM)
genes from genomic libraries.";
Gene 237:61-70(1999)
```

Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

```
Adc19803 Human can
Adc19801 Human can
Adc19793 Human can
Adc19793 Human can
Adc19792 Human can
Adc19792 Human can
Adc19792 Human can
Adc19792 Human can
Adc19795 Human can
Adc19795 Human can
Adc19706 Human PRO
Adac19706 Human BRO
Adac1921 Novel hum
Add76153 Human PRO
Adac1921 Novel hum
Add76153 Human PRO
Adac1921 Novel hum
Add776153 Human PRO
Adac1921 Novel hum
Add77752 CDNA enco
Adac1931 Novel hum
Add77752 CDNA enco
Adac1931 Novel hum
Add57752 CDNA enco
Adac1931 Novel hum
Add57752 Human PRO
Adac191 Human PRO
Aax90699 Human SVP
Abx11650 Human cDN
Aaas9304 DNA encod
Aaas9305 DNA encod
Aaas9306 DNA encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, SVPH1-26; proteinase; testis; fertilisation; spermatogenesis; birth control; detergent additive; diagnosis; testicular cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                         ADC19812
ADC19809
                                                                                                                                                                                                                                                                                                                 AAX28637
AAD21436
                                                                                                                                                                                                                                                                                                                                                                          ADC78910
                                                                                                                                                                                                                                                                             ADC19795
                                                                                                                                                                                                                                                                                                  ADC19806
                                                                                                                ADC19811
                                                                                                                                                                   ADC19805
                                                                                                                                                                                                       ADC19802
                                                                                                                                                                                                                                                                                                                                                                                            AAS21345
     AAX90699
                                                                             AAA59306
                                                                                                                                                                                                                                                                                                                                                         AAA59226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB19211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SVPH1-26 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВБ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX56461 standard; DNA; 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US022965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0063571P.
                                                                                                                                                                                                                                                                                                                                                       3 7
10 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                             2463
2629
2629
2629
5112
5112
6150
6150
6213
6213
1856
1856
                                                                                                                                                                                                                                                                                                                                                       2373
2694
2695
2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-337487/28.
P-PSDB; AAY17413.
     34.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9923228-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999
   2435
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102.5
2102
                                                                                                                                                                                                                                                                                                                                                                                          1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1387.5
                                                                                                                                                                                                                                                                                                                                                       1387.5
                                                                                                                                                                                                                                                                                                                                                                          1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1387.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX5646:
       Command line parameters:
-WODEL=frame+ p2n.model -DEV=x1p
-WODEL=frame+ p2n.model -DEV=x1p
-WODEL=frame+ p2n.model -DEV=x1p
-Cgn2 1/USPTO spool p/US10633202/runat 14062005 141725 13079/app_query.fasta_1.903
-DB=N Geneseq 16Dec04 -QFWN=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human440.cdi
-LIST=45 -DOCALIGN=200 -THR ROCRE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25
-WODBE-LOCAL -OUTPWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10633202 @CGN 1 1 708 @runat 14062005 141725 13079 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG SCORES=0 -WALT -DSPBLOCK=100 -LONCLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREAD=1 -XGAPPP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aax56461 Human SVP
Abz76248 Human GEN
Aax28636 Nucleotid
Adc78876 Human PRO
Ade85180 Farnesyl
                                                                                                                                 June 15, 2005, 20:15:51; Search time 1341 Seconds (without alignments) 3204.871 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                         1 MAVGEPLVHIRVTLLLLWFG......LFCLHVLFKKRTKSKEDEEG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            4390206 segs, 2959870667 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56461
ABZ76248
AAX28636
ADC78876
                                                                                                                                                                                                                                                                                                  0.5
7.0
7.0
                                                                                                                                                                                                                                                                                                  , Xgapext
, Ygapext
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         geneseqn2003cs:*
geneseqn2003ds:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geneseqn2004as:*
geneseqn2004bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         geneseqn2000s:*
geneseqn2001as:*
geneseqn2001bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genesegn2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqn2002as:*
geneseqn2002bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqn2003as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geneseq 16Dec04:*
geneseqn1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          geneseqn1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                         US-10-633-202-2
                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , X
Ygapop 10.0 , Y
Fgapop 6.0 , E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2181
3230
2426
2442
2442
                                           Copyright
                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
99.4
99.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
```

Database :

4030 4004 4004 4004

Result No.

oŧ human SVPH1-26 DNA useful for the diagnosis and prognosis testicular cancers.

Claim 1; Page 70-73; 96pp; English

are proteinases implicated in fertilisation and spermatogenesis. They can be used as therapeutic agents. A proteinase inhibitor of the catalytic domain would inhibit SVPH1-26 activity and would be useful as a method for birth control. Also, an inhibitor of the disintegrin domain of SVPH1-26 may affect fertilisation. The proteinase activity of SVPH1-26 can also be used as a detergent additive for the removal of stains having a protein component. The SVPH1-26 polypeptides and fragments can also be used as molecular weight markers, as markers for determination of isoelectric points of sample proteins and as controls for establishing the extent of fragmentation of a protein sample. The products can also be used for identifying, separating or purifying cells that express SVPH1-26 polypeptides such as testis cells. They can be used for the diagnosis and prognosis of testicular cancers polypeptides encodes human SVPH1-26. Human SVPH1-26 present sequence 

Sequence 2181 BP; 600 A; 423 C; 530 G; 628 T; 0 U; 0 Other;

|  |               | 20  | 09        | 40                                       | 120                                      | 9  | 180   | 80   | 240  | 100  | 300   | 120  | 360  | 140   | 420                                      | 160   | 480  |
|--|---------------|---|-----------|--|--|--|---|--|--|--|---|--|--|---|--|---|--|
| Length: 2181  Matches: 726  Conservative: 0  Mismatches: 0  Indels: 0  Gaps: 0 | 6461 (1-2181) | yGluProLeuValHisIleArgValThrLeuLeuLeuLeuTrpPheGly |           | YHisSerGlnAlaArgProSerGlnTyrPheThrSerPro | AIGTITITITITITITITITITITITITITITITITITIT | SVallleSerArgGlyArgGlyAlaLysAlaProGlyTrp | TGAAGGTGATCAGCAGGGCAGAGGTGCAAAGGCTCCTGGATGG | rSerLeuArgPheGlyGlyGlnArgTyrIleValHisMetArgValAsnLys | CTCTCCTATAGCCTGCGGTTTGGGGGACAGAGATACATTGTCCACATGAGGGTAAATAAG | euProValPheThrTyrThrGluGlnHisAllaLeuLeuGln | CACCTTCTTGTTTCACCTACAGAGCAGCATGCCCTGCTCCTGG | eGlnAspAspCysTyrTyrHisGlyTyrValGluGlyValProGlu | GATCAGCCCTTCATCCAGGATGACTGCTACTACCATGGTTATGTGGGGGGGG | aLeuSerThrCysSerGlyGlyPheLeuGlyMetLeuGlnIleAsnAsp | CTGTTCTGGGGGCTTTCTTGGAATGCTACAGATAAATGAC | BProlleSerValSerAlaThrPheGluHisLeuValTyrLys | CAAGCCAATTAGTGTTTCTGCCACATTTGAACACCTAGTATAAG |
| 0<br>4030.00<br>100.00%<br>100.00%<br>2  | x AAX56461    | GlyGluP   | GGTGAGC   | Seriles                                  | CTATT                                    | IleProLeuLy                              | ATCCCTT                                     | SerLeuA  | AGCCTGC  | AlaAlaH                                    | GCTGCAC                                     | PhelleG  | TTCATCC  |   | SCCTTA                                   | rGlulleLy                                   | GAAATCA                                      |
| res:<br>arity:<br>milarity:  | -2 (1-726)    | MetAlaValGl                                       | ATGGCAGTG | MetPheLeuSerIleSerGl                     | ATGTTTTTG                                | GluValValI                               | GAAGTGGTGAT                                 | LeuSerTyr  | CTCTCCTAT  | LeuLeuPheAlaAlaHisL                        | CTGTTGTTT                                   | AspGlnProPheIl                                 | GATCAGCCC  | SerLeuValAl                                       | TCCTTGGTTGCCCTTAGTAC                     | LeuValTyr                                   | CTTGTTTATGAAAT                               |
| ment Scores No.: it Similari Local Simil: Match:                               | -202          | н   | ч         | 21                                       | 61                                       | 41                                       | 121   | 61   | 181  | 81   | 241   | 101  | 301  | 121   | 361                                      | 141   | 421  |
| Alignment<br>Pred. No.<br>Score:<br>Percent S<br>Best Loca<br>Query Mat<br>DB: | US-10-633     | δ   | q         | ò  | qq                                       | ò  | Ωp  | à  | qq   | à  | qq  | δλ   | qq   | ò   | qq                                       | ò   | đ  |

lleAspSerAspAspThrGlnPheProProMetArgCysGlyLeuThrGluGluLysIle 180

161 481 181

ઠે g 8 8

AlaHisGlnMetGluLeuGlnLeuSerTyrAsnPheThrLeuLysGlnSerPheVal GCACACCAGAIGGAGTIGCAATIGICATATAATITICACTCTGAAGCAAAGTICTITIGIG

540 200 600

| S S        | 201  | GlyTrpTrpThrHisGlnArgPheValGluLeuValValValValAspAsnIleArgTyr 220<br>                                     |
|------------|------|--|
| දු පු      | 221  | LeuPheSerGlnSerAsnAlaThrThrValGlnHisGluValPheAsnValValAsnIle 240   |
| දු පු      | 241  | 241 ValaspserPheTyrHisProLeuGluValaspValIleLeuThrGlylleAspIleTrp 260                                     |
| 8 8        | 261  | ThralaserAsnProLeuProThrSerGlyAspLeuAspAsnValLeuGluAspPheSer 280   |
| 3 &        | 781  | ACIGCALCACALICCIACCAGGGGGGGGCGGGGGGGGGGG   |
| qq         | 841  | ATTIGGAAGAAITATAACCTTAATAATCGACTACAACAIGATGTTGCACATCTTTCATA 900  |
| 상<br>임     | 301  | LysAspThrGlnGlyMetLysLeuGlyValAlaTyrValLysGlyIleCysGlnAsnPro 320   |
| ò          | 321  | PheAsnThrGlyValAspValPheGluAspAsnArgLeuValValPheAlaIleThrLeu 340   |
| qq         | 961  | triaaracigaagrigargrifitaaagacaacaggriggicgrifitigcaarractrig 1020                                       |
| , da       | 341  | GlyHisGluLeuGlyHisAsnLeuGlyMetGlnHisAspThrGlnTrpCysValCysGlu 360   |
| à          | 361  |  |
| e<br>G     | 1081 |  |
| <u>ک</u> خ | 381  | TyralaginTyrTrpAspSerThrIleSerSerGlyLeuCysIleGinProProTyr 400  |
| 3 &        | 401  |  |
| - අ        | 1201 |  |
| ò          | 421  | CysAspCysGlyThrIleArgGlnCysAlaLysAspProCysCysLeuLeuAsnCysThr 440   |
| qq         | 1261 | TGTGACTGTGGAACCATACGGCAGTGTGCAAAGATCCCTGTTGTCTGTTAAACTGTACT 1320   |
| ري<br>و    | 441  | LeuhisProGlyAlaAlaCysAlaPheGlyIleCysCysLysAspCysLysPheLeuPro 460   |
| à          | 461  | SerGlyThrLeuCysArgGlnGlnValGlyGluCysAspLeuProGluTrpCysAsnGly 480   |
| ор         | 1381 | TCAGGAACTTTATGTAGACAACAAGTTGGTGAATGTGACCTTCCAGAGTGGTGCAATGGG 1440  |
| ò          | 481  | ThrSerHisGlnCysProAspAspValTyrValGlnAspGlyIleSerCysAsnValAsn 500   |
| QQ         | 1441 | ACATCCCATCAATGCCCCAGATGTGTGTGTGCCAGGGCGGGATCTCCTGTAATGTGAAT 1500   |
| ò          | 501  |  |
| අු         | 1501 | GCCTTCTGCTATGAAAAGACGTGTAATAACCATGATATACAATGTAAAAGAGATTTTTTGGC 1560                                      |
| <u>ک</u> ځ | 521  | GInAspalaArgSerAlaSerGlnSerCysTyrGlnGlulleAsnThrGlnGlyAsnArg 540 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1] |
| 3 (        | 1961 |  |
| රු දි      | 541  | PheG.yHisCysGlyIleValGlyThrThrTyrValLysCySTrpThrProAsplieMer 560   |
| 3 8        | 561  |  |
|            |      |  |